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1 ACAAGAATCT GCATTACACC ATGTACTTTT TCATCTGTAG CCTGGCTGTG  
51 GCTGATATGC TGGTGAGCGT TTCCAATGGG TCAGAAACCA TTGTCAATCAC  
101 CCTATTAAAC AGCACGGACA CGGACGCACA GAGTTTCACA GTGAATATTG  
151 ATAATGTCAT TGAATCAGTG ATCTGTAGCT CCTTACTCGC CTCGAATTTCG  
201 AGCCTGCTTT CGATTGCAGT GGACAGGTAT TTTTACTATCT TTTATGCTCT  
251 CCAGTACCAT AACATTATGA CAGTTAAGCG GGTGGAATC ATCATCAGTT  
301 GTATCTGGC AGTCTGCACG GTGTCGGGTG TTTTGTTCAT CATTACTCA  
351 GATAGCAGTG CTGTTATTAT CTGCCTCATA ACCGTGTTCT TCACCATGCT  
401 GGCTCTCATG GCTTCTCTCT ATGTCCACAT GTTCCTCAIG GCCAGACTCC  
451 ACATTAAGAG GATCGCCGTC CTCCCAGGCA CTGGCACCAT CCGCCAAGGT  
501 GCCAACATGA AGGGGGCAAT TACCCTGACC ATCTTGATTG GGGTCTTTGT  
551 GGTCTGCTGG GCCCCCTTCT TCCTCCACTT AATATTCTAT ATCTCCTGCC

Fig. 1

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601 CCCAGAAATCC ATACTGTGTG TGCTTCATGT CTCACCTTAA TTTGTATCTC  
651 ATCCTGATCA TGTGTAATC CATCATCXAT CCCCTGATTT ATGCACTCCG  
701 GAGCCAAGAA CTGAGGAAA CCTTCAAAGA GATCATCTGT TGCTAT

Fig. 1A

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con-mc4r.seq      10      20      30
                  ACAAGAATCTGCATTCAACCCATGTACTTTT
s77415           |||||
                  ATATCTTAGTGATTGTGGCAATAGCCAAGAACAAAGAATCTGCATTCAACCCATGTACTTTT
580      590      600      610      620      630

con-mc4r.seq      40      50      60      70      80      90
                  TCATCTGTAGCCCTGGCTGTGGCTGATATGCTGGTGAGCGTTTCCAATGGGTCAGAAACCA
s77415           |||||
                  TCATCTGCAGCTTGGCTGTGGCTGATATGCTGGTGAGCGTTTCCAATGGGTCAGAAACCA
640      650      660      670      680      690

con-mc4r.seq      100     110     120     130     140     150
                  TTGTCATCACCCCTATTAAACAGCACGGACACGGACGACAGAGTTTCACAGTGAATATG
s77415           |||||
                  TTATCATCACCCCTATTAAACAGTACAGATACGGATGACAGAGTTTCACAGTGAATATG
700     710     720     730     740     750

con-mc4r.seq      160     170     180     190     200     210
                  ATAAATGTCATTGACTCAGTGATCTGTAGCTCCTTACTCGCCTCAATTTCAGCCTGCTTT
s77415           |||||
                  ATAAATGTCATTGACTCGGTGATCTGTAGCTCCTTGTGCTTGCATCCATTTCAGCCTGCTTT
760     770     780     790     800     810
```

Fig. 2A

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con-mc4r.seq      220      230      240      250      260      270
CGATTGCAGTGGACAGGTATTTTACTATCTTTTATGCTCTCCAGTACCATTAACATTATGA
|||||
s77415          820      830      840      850      860      870
CAATTGCAGTGGACAGGTACTTTACTATCTTCTATGCTCTCCAGTACCATTAACATTATGA
|||||

con-mc4r.seq      280      290      300      310      320      330
CAGTTAAGCGGGTTGGAATCATCATCAGTTGTATCTGGGCAGTCTGCACGGTGTGCGGTG
|||||
s77415          880      890      900      910      920      930
CAGTTAAGCGGGTTGGGATCAGCATAAAGTTGTATCTGGGCAGCTTGCACGGTTTCAGGCA
|||||

con-mc4r.seq      340      350      360      370      380      390
TTTTGTTCATCATTTTACTCAGATAGCAGTGTCTGTTATATCTGCCCTCATAACCGTGTCT
|||||
s77415          940      950      960      970      980      990
TTTTGTTCATCATTTTACTCAGATAGTAGTGTCTGTATCATCTGCCCTCATCACCATTCT
|||||

con-mc4r.seq      400      410      420      430      440      450
TCACCATGTGGCTCTCATGGCTTCTCTCTATGTCCACATGTTCTCATGGCCAGACTCC
|||||
s77415          1000     1010     1020     1030     1040     1050
TCACCATGTGGCTCTCATGGCTTCTCTCTATGTCCACATGTTCTCATGGCCAGGCTTC
|||||

con-mc4r.seq      460      470      480      490      500      510
ACATTAAGAGGATCGCCGCTCTCCAGGCACCTGGCACCATCCGCCAAGGTGCCAATGA
|||||
s77415          1060     1070     1080     1090     1100     1110
ACATTAAGAGGATTGCTGTCTCTCCCGGCACCTGGTGCCATCCGCCAAGGTGCCAATGA
|||||
```

Fig. 2B

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con-mc4r.seq 520 530 540 550 560 570
AGGGGCAATTACCTGACCATTGATTGGGGCTTTGTGGTCTGCTGGGCCCCCTTCT
|||||
AGGGAGCGATTACCTTGACCATCCTGATTGGCGTCTTTGTTGTCTGCTGGGCCCCATTCT
1120 1130 1140 1150 1160 1170

con-mc4r.seq 580 590 600 610 620 630
TCCTCCACTTAATATCTATATCTCCTGCCCCAGAAATCCATACTGTGTGTGCTTCATGT
|||||
TCCTCCACTTAATATCTATATCTCCTGCCCCAGAAATCCATACTGTGTGTGCTTCATGT
1180 1190 1200 1210 1220 1230

con-mc4r.seq 640 650 660 670 680 690
CTCAGTTTAAATTTGTATCTCATCTGATCATGTGTAATCCATCATCAATCCCCTGATTT
|||||
CTCAGTTTAACTTGTATCTCATCTGATCATGTGTAATCCATCATCAATCCCCTGATTT
1240 1250 1260 1270 1280 1290

con-mc4r.seq 700 710 720 730 740
ATGCACTCCGGAGCCCAAGAACTGAGGAAACCTTCAAAGAGATCATCTGTGTGCTAT
|||||
ATGCACTCCGGAGTCAAGAACTGAGGAAACCTTCAAAGAGATCATCTGTGTGCTATCCCC
1300 1310 1320 1330 1340 1350

s77415 TGGGAGGCCCTTTGTGACTTGTCTAGCAGATATTAATGGGACAGACGCAATATAGG
1360 1370 1380 1390 1400 1410
```

Fig. 2C

Fig. 3A

*Fig. 3B*

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S0082	MC4R	rec. frags.=	0.05,	lods =	14.74
CGA	MC4R	rec. frags.=	0.14,	lods =	6.88
S0020	MC4R	rec. frags.=	0.18,	lods =	5.32
S0079	MC4R	rec. frags.=	0.12,	lods =	10.35
S0155	MC4R	rec. frags.=	0.14,	lods =	7.68
S0122	MC4R	rec. frags.=	0.18,	lods =	5.17
S0313	MC4R	rec. frags.=	0.00,	lods =	17.76
S0312	MC4R	rec. frags.=	0.20,	lods =	5.60
S0311	MC4R	rec. frags.=	0.17,	lods =	7.18
S0416	MC4R	rec. frags.=	0.20,	lods =	3.21
S0331	MC4R	rec. frags.=	0.02,	lods =	21.91
S0396	MC4R	rec. frags.=	0.16,	lods =	7.85
BHT0433	MC4R	rec. frags.=	0.02,	lods =	21.32
S0536	MC4R	rec. frags.=	0.03,	lods =	15.61
CAPN3	MC4R	rec. frags.=	0.12,	lods =	6.65

Fig. 4A



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KGF	MC4R	rec. frags.=	0.09,	lods =	6.46
MEF2A	MC4R	rec. frags.=	0.05,	lods =	14.36
MC4R	MC4R	rec. frags.=	0.00,	lods =	26.19
S0082	MC4R	rec. frags.=	0.00	0.09,	lods = 15.86
CGA	MC4R	rec. frags.=	0.07	0.22,	lods = 7.46
S0020	MC4R	rec. frags.=	0.00	0.25,	lods = 6.33
S0079	MC4R	rec. frags.=	0.00	0.19,	lods = 11.48
S0155	MC4R	rec. frags.=	0.00	0.24,	lods = 9.98
S0122	MC4R	rec. frags.=	0.00	0.27,	lods = 7.10
S0313	MC4R	rec. frags.=	0.00	0.00,	lods = 17.76
S0312	MC4R	rec. frags.=	0.04	0.29,	lods = 7.45

Fig. 4B

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S0311	MC4R	rec.	fracs.=	0.00	0.28,	lods =	9.02
S0416	MC4R	rec.	fracs.=	0.00	0.31,	lods =	4.17
S0331	MC4R	rec.	fracs.=	0.05	0.00,	lods =	22.14
S0396	MC4R	rec.	fracs.=	0.03	0.24,	lods =	9.33
BHT0385	MC4R	rec.	fracs.=	0.14	0.36,	lods =	3.46
BHT0433	MC4R	rec.	fracs.=	0.05	0.00,	lods =	21.82
S0536	MC4R	rec.	fracs.=	0.00	0.05,	lods =	15.77
CAPN3	MC4R	rec.	fracs.=	0.00	0.18,	lods =	7.35
KGF	MC4R	rec.	fracs.=	0.00	0.17,	lods =	6.74
MEF2A	MC4R	rec.	fracs.=	0.10	0.00,	lods =	14.52
MC4R	MC4R	rec.	fracs.=	0.00	0.00,	lods =	26.19

Fig. 4C

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0	ESR			0.0
		0.18	18.4	
1	S0008			18.4
		0.12	11.9	
7	CGA			30.3
		0.03	2.8	
3	S0312			33.1
		0.05	4.9	
4	S0122			38.1
		0.09	9.4	
8	KGF			47.4
		0.06	5.8	
6	CAPN3			53.2
		0.02	2.5	
9	MEF2A			55.7
		0.06	6.1	
5	MC4R			61.8
		0.06	5.6	
10	S0313			67.4
		0.00	0.0	
11	S0082			67.4
		0.03	3.4	
12	S0079			70.8
		0.03	2.5	
14	S0142			73.3
		0.01	1.0	
13	S0020			74.4
		0.04	4.3	
15	S0311			78.7
		0.00	0.0	
16	S0155			78.7
		0.12	12.2	
17	S0113			90.9
		0.20	21.0	
18	S0302			111.9
		0.22	23.4	
19	S0112			135.3

Fig. 4D

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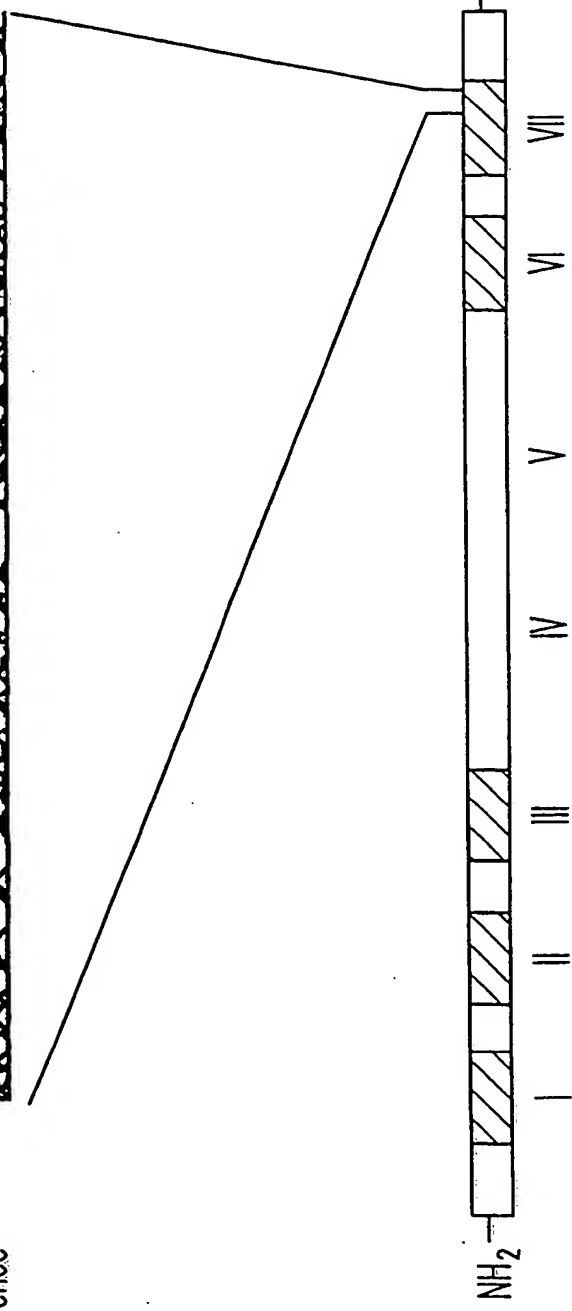
Allele 1  
 homozygote  
 sequence

293 C N S L I D P L I Y  
 295 S L I D P L I Y  
 297  
 299 P L I Y  
 300

GTGTAATTCCATCATCGATCCCTGATTTATGCG

Allele 2  
 homozygote  
 sequence

C N S L I D P L I Y  
 GTGTAATTCCATCATCAATCCCTGATTTATGCG





 = Transmembrane domains

Fig. 5

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pMC4R	.....MSHFNLYL I L I M C N S I I D P L I Y A L..... *
hMC4R	.....MSHFNLYL I L I M C N S I I D P L I Y A L..... 304
rMC4R	.....MSHFNLYL I L I M C N A V I D P L I Y A L..... 304
sheep MC5R	.....MSHFNMYL I L I M C N S V I D P L I Y A..... 286
bovine MC5R	.....MSHFNMYL I L I M C N S V I D P L I Y A..... 286
bovine MC2R	.....M S L F Q V N G V L I M C N A I I D P F I Y A L..... 268
hMC3R	.....A H F N T Y L V L I M C N S V I D P L I Y A..... 327
mMC3R	.....A H F N T Y L V L I M C N S V I D P L I Y A..... 290
hMC2R	.....M S H F N M Y L I L I M C N S V M D P L I Y A..... 268
hMC1R	.....S Y F N L F L I L I I C N S V V D P L I Y A..... 299
bEDG-2R	.....L A Y E K F F L L L A E F N S A M N P I I Y S Y R.... 314
hEDG-4R	.....F L L L A E A N S L V N A A V Y S C R.... 298
human cannab	.....V F A F C S M L C L L N S T V N P L I Y A L..... 399
hH2AB	.....F Q F F W I G Y C N S S L N P V I Y T I..... 290
rSSR2	.....F D F V V I L T Y A N S C A N P I L Y A F L.... 315
hGAL1-R	.....L A Y S N S S V N P I I Y A F L.... 306

*Fig. 6*